

ABSTRACT

A search method in a biological sample containing an HIV 2 viral strain for possible resistance of said strain to treatment by an anti-protease agent, and nucleotide probes for the implementation thereof. According to methods known per se, the presence of at least one mutation at certain, specified, particular positions of the proteinic sequence of the protease of said viral strain from a biological sample taken from a patient contaminated by HIV 2 is searched. If said mutation is observed, the existence of a resistance to said anti-protease agent is assumed in the patient.